

FIGURE 1

cDNA sequence of wild type amFP486

ATGGCTCTTTCAAACAAGTTTATCGGAGATGACATGAAAATGACCTACCATATGGATG  
GCTGTGTCAATGGGCATTACTTTACCGTCAAAGGTGAAGGCAACGGGAAGCCATACGA  
AGGGACGCAGACCTCGACTTTTAAAGTCACCATGGCCAACGGTGGGCCCCTTGCATTC  
TCCTTTGACATACTATCTACAGTGTTCAAGTATGGAAATCGATGCTTTACTGCGTATC  
CTACCAGTATGCCCAGCTATTTCAAACAAGCATTTCTGACGGAATGTCATATGAAAG  
GACTTTTACCTATGAAGATGGAGGAGTTGCTACAGCCAGTTGGGAAATAAGCCTTAAA  
GGCAACTGCTTTGAGCACAAATCCACGTTTCATGGAGTGAACTTTCCTGCTGATGGAC  
CTGTGATGGCGAAGATGACAACTGGTTGGGACCCATCTTTTGAGAAAATGACTGTCTG  
CGATGGAATATTGAAGGGTGATGTCACCGCGTTCCTCATGCTGCAAGGAGGTGGCAAT  
TACAGATGCCAATTCCACACTTCTTACAAGACAAAAAACCAGGTGACGATGCCACCAA  
ACCATGCGGTGGAACATCGCATTTGCGAGGACCGACCTTGACAAAGGTGGCAACAGTGT  
TCAGCTGACGGAGCACGCTGTTGCACATATAACCTCTGTTGTCCCTTTC (SEQ ID  
NO:01)

amino acid sequence of wild type amFP486

MALSNKFIGD DMKMTYHMDG CVNGHYFTVK GEGNGKPYEG TQTSTFKVTM ANGGPLAFSF  
DILSTVFKYG NRCFTAYPTS MPDYFKQAFP DGMSYERTFT YEDGGVATAS WEISLKGNCF  
EHKSTFHGVN FPDGPMVMAK MTTGWDPSFE KMTVCDGILK GDVTAFLMLQ GGGNYRCQFH  
TSYKTKKPVT MPPNHAVEHR IARTDLKGG NSVQLTEHAV AHITSVVPF  
(SEQ ID NO:02)

cDNA sequence of wild type cFP484

amino acid sequence of wild type cFP484

M	K	C	K	F	V	F	C	L	S								
F	L	V	L	A	I	T	N	A	N	I	F	L	R	N	E	A	D
E	K	T	L	R	I	P	K	A	L	T	T	M	G	V	I	K	P
K	I	K	L	K	M	E	G	N	V	N	G	H	A	F	V	I	E
G	E	G	K	P	Y	D	G	T	H	T	L	N	F	V	K	E	G
P	L	P	F	S	Y	D	I	L	S	N	A	N	Q	Y	G	N	R
T	K	Y	P	D	D	I	A	D	Y	F	K	Q	S	F	P	E	G
W	E	R	T	M	T	F	E	D	K	G	I	V	K	V	K	S	D
M	E	E	D	S	F	I	Y	E	I	R	F	D	G	M	N	F	P
G	P	V	M	Q	K	K	T	L	K	W	E	P	S	T	E	I	M
R	D	G	V	L	V	G	D	I	S	H	S	L	L	L	E	G	G
Y	R	C	D	F	K	S	I	Y	K	A	K	K	V	V	K	L	P
H	F	V	D	H	R	I	E	I	L	N	H	D	K	D	Y	N	K
L	Y	E	N	A	V	A	R	Y	S	L	L	P	S	Q	A	(SEQ ID NO: 04)	

Figure 3

cDNA sequence of zFP506

ATGGCTCAGTCAAAGCACGGTCTAACAAAAGAAATGACAATGAAATACCGTATGGAAGGGTGC  
GTCGATGGACATAAATTTGTGATCACGGGAGAGGGCATTGGATATCCGTTCAAAGGGAAACAG  
GCTATTAATCTGTGTGTGGTTCGAAGGTGGACCATTTGCCATTTGCCGAAGACATATTGTCAGCT  
GCCTTTATGTACGGAAACAGGGTTTTCTACTGAATATCCTCAAGACATAGCTGACTATTTCAAG  
AACTCGTGTCTGCTGGTTATACATGGGACAGGTCTTTTCTCTTTGAGGATGGAGCAGTTTGC  
ATATGTAATGCAGATATAACAGTGAGTGTTGAAGAAAACATGCATGTATCATGAGTCCAAATTT  
TATGGAGTGAATTTTCTGCTGATGGACCTGTGATGAAAAAGATGACAGATAACTGGGAGCCA  
TCCTGCGAGAAGATCATAACAGTACCTAAGCAGGGGATATTGAAAGGGGATGTCTCCATGTAC  
CTCCTTCTGAAGGATGGTGGGCGTTTACGGTGCCAATTCGACACAGTTTACAAAGCAAAGTCT  
GTGCCAAGAAAGATGCCGGACTGGCACTTCATCCAGCATAAGCTCACCCGTGAAGACCGCAGC  
GATGCTAAGAATCAGAAATGGCATCTGACAGAACATGCTATTGCATCCGGATCTGCATTGCCC  
(SEQ ID NO:05)

amino acid sequence of zFP506

MAQSKHGLTK EMTMKYRMEG CVDGHKPVIT GEGIGYPFKG KQAINLCVVE GGPLPFAEDI LSAAFNYGNR VFTEYPQDIA  
DYFKNSCPAG YTWDRSFLFE DGAVCICNAD ITVSVEENCM YHESKFYGVN FPADGPVMKK MTDNWEPSCE KIIPVPKQGI  
LKGDVSMYLL LKDGGRRLRCQ FDTVYKAKSV PRKMPDWHFI QHKLTREDRS DAKNQKWHLT EHAIASGSAL P  
(SEQ ID NO:06)

F04027-226900F

Figure 4

## cDNA sequence of zFP538

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gagttgagtt tctcgacttc agttgtatca attttggggc atcaagcgat ctattttcaa
catggctcat tcaaagcacg gtctaaaaga agaaatgaca atgaaatacc acatggaagg
gtgctgaac ggacataaat ttgtgatcac gggcgaaggc attggatata cgttcaaagg
gaaacagact attaattctgt gtgtgatcga agggggacca ttgccatttt ccgaagacat
attgtcagct ggctttaagt acggagacag gatttttact gaatatacctc aagacatagt
agactatttc aagaactcgt gtcctgctgg atatacatgg ggcagggtctt ttctctttga
ggatggagca gtctgcatat gcaatgtaga tataacagtg agtgtcaaag aaaactgcat
ttatcataag agcatattta atggaatgaa ttttctgct gatggacctg tgatgaaaaa
gatgacaact aactgggaag catcctgcga gaagatcatg ccagtaccta agcaggggat
actgaaaggg gatgtctcca tgtacctcct tctgaaggat ggtggggtgtt accggtgcca
gttcgacaca gtttacaaag caaagtctgt gccaaagtaag atgccggagt ggcacttcat
ccagcataag ctctccgtg aagaccgcag cgatgctaag aatcagaagt ggcagctgac
agagcatgct attgcattcc cttctgcctt ggcttgataa gaatgtagtt ccaacatttt
aatgcatgtg cttgtcaatt attctgataa aaatgtagtt gagttgaaaa cagacaagta
caaataaagc acatgtaaat cgtct      (SEQ ID NO:07)

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## amino acid sequence of zFP538

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Met Ala His Ser Lys His Gly Leu Lys Glu Glu Met Thr Met Lys
Tyr His Met Glu Gly Cys Val Asn Gly His Lys Phe Val Ile Thr
Gly Glu Gly Ile Gly Tyr Pro Phe Lys Gly Lys Gln Thr Ile Asn
Leu Cys Val Ile Glu Gly Gly Pro Leu Pro Phe Ser Glu Asp Ile
Leu Ser Ala Gly Phe Lys Tyr Gly Asp Arg Ile Phe Thr Glu Tyr
Pro Gln Asp Ile Val Asp Tyr Phe Lys Asn Ser Cys Pro Ala Gly
Tyr Thr Trp Gly Ser Phe Leu Phe Glu Asp Gly Ala Val Cys Ile
Cys Asn Val Asp Ile Thr Val Ser Val Lys Glu Asn Cys Ile Tyr
His Lys Ser Ile Phe Asn Gly Met Asn Phe Pro Ala Asp Gly Pro
Val Met Lys Lys Met Thr Thr Asn Trp Glu Ala Ser Cys Glu Lys
Ile Met Pro Val Pro Lys Gln Gly Ile Leu Lys Gly Asp Val Ser
Met Tyr Leu Leu Leu Lys Asp Gly Gly Arg Tyr Arg Cys Gln Phe
Asp Thr Val Tyr Lys Ala Lys Ser Val Pro Ser Lys Met Pro Glu
Trp His Phe Ile Gln His Lys Leu Leu Arg Glu Asp Arg Ser Asp
Ala Lys Asn Gln Lys Trp Gln Leu Thr Glu His Ala Ile Ala Phe
Pro Ser Ala Leu Ala (SEQ ID NO:08)

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10006922-120401

FIGURE 5

cDNA sequence of dsFP483

ACGGTCAGGGACACGGTGACCCACTTTGGTATTCTAACAAAATGAGTTGGTCCAAGAGTG  
TGATCAAGGAAGAAATGTTGATCGATCTTCATCTGGAAGGAACGTTCAATGGGCACTACT  
TTGAAATAAAAGGCAGGAAAAGGGAAGCCTAATGAAGGCACCAATACCGTCACGCTCG  
AGGTTACCAAGGGTGGACCTCTGCCATTTGGTTGGCATATTTTGTGCCCACAATTTCACT  
ATGGAAACAAGGCATTTGTCCACCACCCTGACGACATACCTGATTATCTAAAGCTGTCAT  
TTCCGGAGGGATATACATGGGAACGGTCCATGCACCTTTGAAGACGGTGGCTTGTGTTGTA  
TCACCAATGATATCAGTTTGACAGGCAACTGTTTCAACTACGACATCAAGTTCACGTGGCT  
TGAACCTTCCTCCAAATGGACCCGTTGTGCAGAAGAAGACAACCTGGCTGGGAACCGAGCA  
CTGAGCGTTTGTATCCTCGTGATGGCGTGTGATAGGAGACATCCATCATGCTCTCACAG  
TGGAAGGAGGTGGTCATTACGTATGTGACATTAATACTGTTTACAGGGCCAAGAAGCCCG  
TAAAGATGCCAGGGTATCACTATGTTGACACCAAACTGGTTATAAGGAGCAACGACAAAAG  
AATTCATGAAAGTTGAGGAGCATGAAATCGCCGTTGCACGCCACCATCCGCTCCAAAGCC  
AATGAAGCTTAAGTAAAGCAAAAAGGTGACGAGGCATGATAGTATGACATGATAGTATGA  
CATGATAGTATGACATGATAGTAAGAATTGTAAGCAAAAAGGCTTTGCTTATTAACTTGT  
AATTGAAAAC (SEQ ID NO:09)

amino acid sequence of dsFP483

M S W S K S V  
I K E E M L I D L H L E G T F N G H Y F  
E I K G K G K G K P N E G T N T V T L E  
V T K G G P L P F G W H I L C P Q F Q Y  
G N K A F V H H P D D I P D Y L K L S F  
P E G Y T W E R S M H F E D G G L C C I  
T N D I S L T G N C F N Y D I K F T G L  
N F P P N G P V V Q K K T T G W E P S T  
E R L Y P R D G V L I G D I H H A L T V  
E G G G H Y V C D I K T V Y R A K K P V  
K M P G Y H Y V D T K L V I R S N D K E  
F M K V E E H E I A V A R H H P L Q S Q  
(SEQ ID NO:10)

10006922 "120491  
T04022" 2260001

FIGURE 6

## cdNA sequence of drFP583

ATGAGGTCTTCCAAGAATGTTATCAAGGAGTTTCATGAGGTTTAAAGGTTTCGCATGGAAGGAACGGTCAATGGGCACGAGT  
 TTGAAATAGAAGGCGAAGGAGAGGGGAGGCCATACGAAGGCCACAATACCGTAAAGCTTAAGGTAACCAAGGGGGGACC  
 TTTGCCATTTGCTTGGGATATTTTGTCAACACAATTTTCAGTATGGAAGCAAGGTATATGTCAAGCACCTGCGGACATA  
 CCAGACTATAAAAAGCTGTCAATTTCTGAAGGATTTAAATGGGAAAGGGTCATGAACCTTTGAAGACGGTGGCGTCGTTA  
 CTGTAACCCAGGATTCAGTTTGCAGGATGGCTGTTTCATCTACAAGGTCAAGTTTCATTGGCGTGAACCTTCCTTCCGA  
 TGGACCTGTTATGCAAAAAGAAGACAATGGGCTGGGAAGCCAGCACTGAGCGTTTGTATCCTCGTGATGGCGTGTGAAA  
 GGAGAGATTATAAGGCTCTGAAGCTGAAAGACGGTGGTCATTACCTAGTTGAATTCAAAGTATTTACATGGCAAAGA  
 AGCCTGTGCAGCTACCAGGGTACTACTATGTTGACTCCAACTGGATATAACAAGCCACAACGAAGACTATACAATCGT  
 TGAGCAGTATGAAAGAACCGAGGGACGCCACCATCTGTTCCTTTAA (SEQ ID NO:11)

## cdNA sequence of drFP583.1

GTCCTCCCAAGCAGTGGTATCAACGCAGAGTACGGGGGAGTTTCAGCCAGTGACGGT  
 CAGTGACAGGGTGAGCCACTTGGTATACCAACAAAATGAGGTCTTCCAAGAATGTTA  
 TCAAGGAGTTTCATGAGGTTTAAAGGTTTCGCATGGAAGGAACGGTCAATGGGCACGAGT  
 TTGAAATAGAAGGCGAAGGAGAGGGGAGGCCATACGAAGGCCACAATACCGTAAAGC  
 TTAAGGTAACCAAGGGGGGACCTTTGCCATTTGCTTGGGATATTTTGTCAACACAAT  
 TTCAGTATGGAAGCAAGGTATATGTCAAGCACCTTGCCGACATACCAGACTATAAAA  
 AGCTGTCAATTTCTGAAGGATTTAAATGGGAAAGGGTCATGAACCTTTGAAGACGGTG  
 GCGTCGTTACTGTAACCCAGGATTCCAGTTTGCAGGATGGCTGTTTCATCTACAAGT  
 CAAGTTTCATTGGCGTTGAACCTTTCTTCCGATGGACCTGTTATGCAAAAAGAAGACAA  
 TGGGCTGGGAAGCCAGCACTGAGCGTTTGTATCCTCGTGATGGCGTGTGAAAGGAG  
 AGATTATAAGGCTCTGAAGCTGAAAGACGGTGGTCATTACCTAGTTGAATTCAAAA  
 GTATTTACATGGCAAAGAAGCCTGTGCAGCTACCAGGGTACTACTATGTTGACTCCA  
 AACTGGATATATAACAAGCCACAACGAAGACTATACAATCGTTGAGCAGTATGAAAGAA  
 CCGAGGGACGCCACCATCTGTTTCTTTAAGGCTGAACCTGGCTCAGACGTGGGTGAG  
 CGGTAATGACCACAAAAGGCAGCGAAGAAAAACCATGATCGTTTTTTTTAGGTTGGC  
 AGCCTGAAATCGTAGGAAATACATCAGAAATGTTACAAACAGG (SEQ ID NO:45)

## amino acid sequence of drFP583

MRSSKNVIKEFMRFKVRMEGTVNGHEFEIEGEGEGRPYEGHNTVKLKVTKGGPLPFAWDILSPQFQ  
 YGSKVYVKHPADIPDYKKLSFPEGFKWERVMNFEDGGVVTVTQDSSLQDGCIFYKVKFIGVNFPSD  
 GPMVMQKKTMGWEASTERLYPRDGVLKGEIHKALKLKDGGHYLVEFKSIYMAKKPVQLPGYYYYVDSK  
 LDITSHNEDYTIVEQYERTEGRHHLFL SEQ ID NO:012)

## amino acid sequence of drFP583.1

Met Arg Ser Ser Lys Asn Val Ile Lys Glu Phe Met Arg Phe Lys  
 Val Arg Met Glu Gly Thr Val Asn Gly His Glu Phe Glu Ile Glu  
 Gly Glu Gly Glu Gly Arg Pro Tyr Glu Gly His Asn Thr Val Lys  
 Leu Lys Val Thr Lys Gly Gly Pro Leu Pro Phe Ala Trp Asp Ile  
 Leu Ser Pro Gln Phe Gln Tyr Gly Ser Lys Val Tyr Val Lys His  
 Pro Ala Asp Ile Pro Asp Tyr Lys Lys Leu Ser Phe Pro Glu Gly  
 Phe Lys Trp Glu Arg Val Met Asn Phe Glu Asp Gly Gly Val Val  
 Thr Val Thr Gln Asp Ser Ser Leu Gln Asp Gly Cys Phe Ile Tyr  
 Lys Ser Ser Ser Leu Ala Leu Asn Phe Pro Ser Asp Gly Pro Val  
 Met Gln Lys Lys Thr Met Gly Trp Glu Ala Ser Thr Glu Arg Leu  
 Gly His Tyr Leu Val Glu Phe Lys Ser Ile Ile Met Ala Lys Lys  
 Pro Val Gln Leu Pro Gly Tyr Tyr Tyr Val Asp Ser Lys Leu Asp  
 Ile Thr Ser His Asn Glu Asp Tyr Thr Ile Val Glu Gln Tyr Glu  
 Arg Ser Glu Gly Arg His His Leu Phe Leu  
 (SEQ ID NO:46)

## Amino Acid and Nucleotide Sequence for asFP600

Amino acid

MASFLKKTMP FKTITIEGTVN GHYFKCTGKG EGNPFEGTQE MKIEVIEGGP LPFAFHILST  
SCMYGSKTFI KYVSGIPDYF QQSFPEGFTW ERTTTYEDGG FLTAHQDTSL DGDCLVYKVK  
ILGNNFPADG PVMQNKAGRW EPATEIVYEV DGVLRGQSLM ALKCPGGRHL TCHLHTTYRS  
KKPAAALKMP GFHFEDHRIE IMEEVEKGKC YKQYEAAGR YCDAAPSKLG HN (SEQ ID  
NO:14)

Figure 8

## cdNA sequence of dgFP512

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attcacctcg gtgatttgta agagaaagga tcaccatcaa gagaagagct gtaaaagtta 60
atattttact gtactttctac cagcatgagt gcacttaaag aagaaatgaa aatcaacctt 120
acaatggaag gtgttggttaa cgggcttcca tttaagatcc gtggggatgg aaaaggcaaa 180
ccataccagg gatcacagga gttaaccttg acggtggtta aaggcggggc tctgcctttc 240
tcttatgata ttctgacaac gatgtttcag tacggcaaca gggcattcgt aaactaccca 300
gaggacatac cagatatttt caagcagacc tgttctggtc ctaatggtgg atattcctgg 360
caaaggacca tgacttatga agacggaggc gtttgcaactg ctacaagcaa catcagcgtg 420
gttgggcgaca ctttcaatta tgacattcac tttatgggag cgaattttcc tcttgatggg 480
ccagtgatgc agaaaagaac aatgaaatgg gaaccatcca ctgagataat gtttgaacgt 540
gatggaatgc tgaggggtga cattgccatg tctctgttgc tgaagggagg gggccattac 600
cgatgtgatt ttgaaactat ttataaaccc aataagggtt tcaagatgcc agattaccat 660
tttgtggacc actgcattga gataacgagt caacaggatt attacaacgt ggttgagctg 720
accgaggttg ctgaagcccg ctactcttcg ctggagaaaa tcggcaaadc aaaggcgtaa 780
atccaagcaa tctaagaaaa caacaaggca ttaaaccgaa tcaccgtttt gaatttttcg 840
ttcgggaattt cttggtaaaa ctaggttttag aacgtttcat ttcgctggac ttctttgact 900
cagctgtaga caagaaaga (SEQ ID NO:15) 919

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## amino acid sequence of dgFP512

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Met Ser Ala Leu Lys Glu Glu Met Lys Ile Asn Leu Thr Met Glu
Gly Val Val Asn Gly Leu Pro Phe Lys Ile Arg Gly Asp Gly Lys
Gly Lys Pro Tyr Gln Gly Ser Gln Glu Leu Thr Leu Thr Val Val
Lys Gly Gly Pro Leu Pro Phe Ser Tyr Asp Ile Leu Thr Thr Met
Phe Gln Tyr Gly Asn Arg Ala Phe Val Asn Tyr Pro Glu Asp Ile
Pro Asp Ile Phe Lys Gln Thr Cys Ser Gly Pro Asn Gly Gly Tyr
Ser Trp Gln Arg Thr Met Thr Tyr Glu Asp Gly Gly Val Cys Thr
Ala Thr Ser Asn Ile Ser Val Val Gly Asp Thr Phe Asn Tyr Asp
Ile His Phe Met Gly Ala Asn Phe Pro Leu Asp Gly Pro Val Met
Gln Lys Arg Thr Met Lys Trp Glu Pro Ser Thr Glu Ile Met Phe
Glu Arg Asp Gly Met Leu Arg Gly Asp Ile Ala Met Ser Leu Leu
Leu Lys Gly Gly Gly His Tyr Arg Cys Asp Phe Glu Thr Ile Tyr
Lys Pro Asn Lys Val Val Lys Met Pro Asp Tyr His Phe Val Asp
His Cys Ile Glu Ile Thr Ser Gln Gln Asp Tyr Tyr Asn Val Val
Glu Leu Thr Glu Val Ala Glu Ala Arg Tyr Ser Ser Leu Glu Lys
Ile Gly Lys Ser Lys Ala
(SEQ ID NO:16)

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FIGURE 9

cDNA sequence of dmFP592

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agtttcagcc agtgacaggg tgagctgcc aagtattctaa caagatgagt tgttccaaga 60
atgtgatcaa ggagttcatg aggttcaagg ttcgtatgga aggaacgggc aatggggcacg 120
agtttgaaat aaaaggcgaa ggtgaagggg ggccttacga aggtcactgt tccgtaaagc 180
ttatggtaac caaggttgga cctttgccat ttgcttttga tattttgtca ccacaatttc 240
agtatggaag caaggtatat gtcaaacacc ctgccgacat accagactat aaaaagctgt 300
catttcctga gggatttaaa tgggaaaggg tcatgaactt tgaagacggg ggcgtgggta 360
ctgtatccca agattccagt ttgaaagacg gctgtttcat ctacgagggc aagttcattg 420
gggtgaactt tccttctgat ggacctgtta tgcagaggag gacacggggc tgggaagcca 480
gctctgagcg tttgtatcct cgtgatgggg tgctgaaagg agacatccat atggctctga 540
ggctggaagg aggcggccat tacctcgttg aattcaaaag tatttacatg gtaaagaagc 600
cttcagtga gttgccaggc tactattatg ttgactccaa actggatatg acgagccaca 660
acgaagatta cacagtcgtt gagcagtatg aaaaaacca gggacgccac catccgttca 720
ttaagcctct gcagtgaact cggctcagtc atggattagc ggtaatggcc acaaaaggca 780
cgatgatcgt tttttaggaa tgcagccaaa aattgaaggt tatgacagta gaaatacaag 840
caacaggctt tgcttattaa acatgtaatt gaaaac 876

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(SEQ ID NO:17)

amino acid sequence of dmFP592

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Met Ser Cys Ser Lys Asn Val Ile Lys Glu Phe Met Arg Phe Lys
Val Arg Met Glu Gly Thr Val Asn Gly His Glu Phe Glu Ile Lys
Gly Glu Gly Glu Gly Arg Pro Tyr Glu Gly His Cys Ser Val Lys
Leu Met Val Thr Lys Gly Gly Pro Leu Pro Phe Ala Phe Asp Ile
Leu Ser Pro Gln Phe Gln Tyr Gly Ser Lys Val Tyr Val Lys His
Pro Ala Asp Ile Pro Asp Tyr Lys Lys Leu Ser Phe Pro Glu Gly
Phe Lys Trp Glu Arg Val Met Asn Phe Glu Asp Gly Gly Val Val
Thr Val Ser Gln Asp Ser Ser Leu Lys Asp Gly Cys Phe Ile Tyr
Glu Val Lys Phe Ile Gly Val Asn Phe Pro Ser Asp Gly Pro Val
Met Gln Arg Arg Thr Arg Gly Trp Glu Ala Ser Ser Glu Arg Leu
Tyr Pro Arg Asp Gly Val Leu Lys Gly Asp Ile His Met Ala Leu
Arg Leu Glu Gly Gly Gly His Tyr Leu Val Glu Phe Lys Ser Ile
Tyr Met Val Lys Lys Pro Ser Val Gln Leu Pro Gly Tyr Tyr Tyr
Val Asp Ser Lys Leu Asp Met Thr Ser His Asn Glu Asp Tyr Thr
Val Val Glu Gln Tyr Glu Lys Thr Gln Gly Arg His His Pro Phe
Ile Lys Pro Leu Gln

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(SEQ ID NO:18)

T00069222120401

Figure 10

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      M   A   L   S   N   E   F   I   G   D   D   M   K   M
676   ATG GCC CTG TCC AAC GAG TTC ATC GGC GAC GAC ATG AAG ATG
      TAC CGG GAC AGG TTG TTC AAG TAG CCG CTG CTG TAC TTC TAC
      T   Y   H   M   D   G   C   V   N   G   H   Y   F   T   V
721   ACC TAC CAC ATG GAC GGC TGC GTG AAC GGC CAC TAC TTC ACC GTG
      TGG ATG GTG TAC CTG CCG ACG CAC TTG CCG GTG ATG AAG TGG CAC
      K   G   E   G   S   G   K   P   Y   E   G   T   Q   T   S
766   AAG GGC GAG GGC AGC GGC AAG CCC TAC GAG GGC ACC CAG ACC TCC
      TTC CCG CTC CCG TCG CCG TTC GGG ATG CTC CCG TGG GTC TGG AGG
      T   F   K   V   T   M   A   N   G   G   P   L   A   F   S
811   ACC TTC AAG GTG ACC ATG GCC AAC GGC GGC CCC CTG GCC TTC TCC
      TGG AAG TTC CAC TGG TAC CGG TTG CCG CCG GGG GAC CGG AAG AGG
      F   D   I   L   S   T   V   F   M   Y   G   N   R   C   F
856   TTC GAC ATC CTG TCC ACC GTG TTC ATG TAC GGC AAC CGC TGC TTC
      AAG CTG TAG GAC AGG TGG CAC AAG TAC ATG CCG TTG GCG ACG AAG
      T   A   Y   P   T   S   M   P   D   Y   F   K   Q   A   F
901   ACC GCC TAC CCC ACC AGC ATG CCC GAC TAC TTC AAG CAG GCC TTC
      TGG CGG ATG GGG TGG TCG TAC GGG CTG ATG AAG TTC GTC CGG AAG
      P   D   G   M   S   Y   E   R   T   F   T   Y   E   D   G
946   CCC GAC GGC ATG TCC TAC GAG AGA ACC TTC ACC TAC GAG GAC GGC
      GGG CTG CCG TAC AGG ATG CTC TCT TGG AAG TGG ATG CTC CTG CCG
      G   V   A   T   A   S   W   E   I   S   L   K   G   N   C
991   GGC GTG GCC ACC GCC AGC TGG GAG ATC AGC CTG AAG GGC AAC TGC
      CCG CAC CGG TGG CGG TCG ACC CTC TAG TCG GAC TTC CCG TTG ACG
      F   E   H   K   S   T   F   H   G   V   N   F   P   A   D
1036  TTC GAG CAC AAG TCC ACC TTC CAC GGC GTG AAC TTC CCC GCC GAC
      AAG CTC GTG TTC AGG TGG AAG GTG CCG CAC TTG AAG GGG CGG CTG
      G   P   V   M   A   K   K   T   T   G   W   D   P   S   F
1081  GGC CCC GTG ATG GCC AAG AAG ACC ACC GGC TGG GAC CCC TCC TTC
      CCG GGG CAC TAC CGG TTC TTC TGG TGG CCG ACC CTG GGG AGG AAG
      E   K   M   T   V   C   D   G   I   L   K   G   D   V   T
1126  GAG AAG ATG ACC GTG TGC GAC GGC ATC TTG AAG GGC GAC GTG ACC
      CTC TTC TAC TGG CAC ACG CTG CCG TAG AAC TTC CCG CTG CAC TGG
      A   F   L   M   L   Q   G   G   G   N   Y   R   C   Q   F
1171  GCC TTC CTG ATG CTG CAG GGC GGC GGC AAC TAC AGA TGC CAG TTC
      CGG AAG GAC TAC GAC GTC CCG CCG CCG TTG ATG TCT ACG GTC AAG
      H   T   S   Y   K   T   K   K   P   V   T   M   P   P   N
1216  CAC ACC TCC TAC AAG ACC AAG AAG CCC GTG ACC ATG CCC CCC AAC
      GTG TGG AGG ATG TTC TGG TTC TTC GGG CAC TGG TAC GGG GGG TTG
      H   V   V   E   H   R   I   A   R   T   D   L   D   K   G
1261  CAC GTG GTG GAG CAC CGC ATC GCC AGA ACC GAC CTG GAC AAG GGC
      GTG CAC CAC CTC GTG GCG TAG CGG TCT TGG CTG GAC CTG TTC CCG
      G   N   S   V   Q   L   T   E   H   A   V   A   H   I   T
1306  GGC AAC AGC GTG CAG CTG ACC GAG CAC GCC GTG GCC CAC ATC ACC
      CCG TTG TCG CAC GTC GAC TGG CTC GTG CGG CAC CGG GTG TAG TGG
      S   V   V   P   F   *
1351  TCC GTG GTG CCC TTC TGA
      AGG CAC CAC GGG AAG ACT

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(SEQ ID NO:27 &amp; 28)

10006923-120401

Figure 11

Non-aggregating mutant FP3-NA was generated from zFP506-N65M (non-humanized version). In comparison with zFP506-N65M, FP3-NA contains two additional amino acid substitutions - K5E and K10E. Also, one accidental nucleotide substitution was introduced due to PCR mistake (double underline).

Cloning into pQE30 was done using BamHI and HindIII sites:

```

GGA TCC GCT CAG TCA GAG CAC GGT CTA ACA GAA GAA ATG ACA ATG AAA
BamHI  A  Q  S  E  H  G  L  T  E  E  M  T  M  K

TAC CGT ATG GAA GGG TGC GTC GAT GGA CAT AAA TTT GTG ATC ACG GGA
Y  R  M  E  G  C  V  D  G  H  K  F  V  I  T  G

GAG GGC ATT GGA TAT CCG TTC AAA GGG AAA CAG GCT ATT AAT CTG TGT
E  G  I  G  Y  P  F  K  G  K  Q  A  I  N  L  C

GTG GTC GAA GGT GGA CCA TTG CCA TTT GCC GAA GAC ATA TTG TCA GCT
V  V  E  G  G  P  L  P  F  A  E  D  I  L  S  A

GCC TTT ATG TAC GGA AAC AGG GTT TTC ACT GAA TAT CCT CAA GAC ATA
A  F  M  Y  G  N  R  V  F  T  E  Y  P  Q  D  I

GTT GAC TAT TTC AAG AAC TCG TGT CCT GCT GGA TAT ACA TGG GAC AGG
V  D  Y  F  K  N  S  C  P  A  G  Y  T  W  D  R

TCT TTT CTC TTT GAG GAT GGA GCA GTT TGC ATA TGT AAT GCA GAT ATA
S  F  L  F  E  D  G  A  V  C  I  C  N  A  D  I

ACA GTG AGT GTT GAA GAA AAC TGC ATG TAT CAT GAG TCC AAA TTC TAT
T  V  S  V  E  E  N  C  M  Y  H  E  S  K  F  Y

GGA GTG AAT TTT CCT GCT GAT GGA CCT GTG ATG AAA AAG ATG ACA GAT
G  V  N  F  P  A  D  G  P  V  M  K  K  M  T  D

AAC TGG GAG CCA TCC TGC GAG AAG ATC ATA CCA GTA CCT AAG CAG GGG
N  W  E  P  S  C  E  K  I  I  P  V  P  K  Q  G

ATA TTG AAA GGG GAT GTC TCC ATG TAC CTC CTT CTG AAG GAT GGT GGG
I  L  K  G  D  V  S  M  Y  L  L  L  K  D  G  G

CGT TTA CGG TGC CAA TTC GAC ACA GTT TAC AAA GCA AAG TCT GTG CCA
R  L  R  C  Q  F  D  T  V  Y  K  A  K  S  V  P

AGA AAG ATG CCG GAC TGG CAC TTC ATC CAG CAT AAG CTC ACC CGT GAA
R  K  M  P  D  W  H  F  I  Q  H  K  L  T  R  E

GAC CGC AGC GAT GCT AAG AAT CAG AAA TGG CAT CTG ACA GAA CAT GCT
D  R  S  D  A  K  N  Q  K  W  H  L  T  E  H  A

ATT GCA TCC GGA TCT GCA TTG CCC TGA AAGCTT
I  A  S  G  S  A  L  P  * HindIII (SEQ ID NO:29 & 30)

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T04027-2259007

Variable	Mean	SD	Min	Max
Age	35.2	10.5	20	55
Gender	Male	10.2	0	20
Marital status	Married	15.8	0	30
Education	High school	12.5	0	25
Occupation	Manager	18.3	0	35
Income	\$30,000	15.0	0	50
Health status	Good	10.0	0	20
Stress level	Low	5.0	0	10
Life satisfaction	High	15.0	0	30
Work-life balance	Good	10.0	0	20
Family size	2.5	1.0	0	5
Home ownership	Owned	15.0	0	30
Commute time	30 min	10.0	0	60
Neighborhood safety	High	10.0	0	20
Public services	Good	10.0	0	20
Crime rate	Low	5.0	0	10
Environmental quality	High	10.0	0	20
Healthcare access	Good	10.0	0	20
Job security	High	10.0	0	20
Retirement savings	High	10.0	0	20
Charitable giving	High	10.0	0	20
Volunteer work	High	10.0	0	20
Community involvement	High	10.0	0	20
Local government	Good	10.0	0	20
Transportation	Good	10.0	0	20
Recreation	Good	10.0	0	20
Food security	High	10.0	0	20
Water quality	High	10.0	0	20
Air quality	High	10.0	0	20
Climate change	High	10.0	0	20
Disaster preparedness	High	10.0	0	20
Emergency services	Good	10.0	0	20
Public safety	Good	10.0	0	20
Law enforcement	Good	10.0	0	20
Judicial system	Good	10.0	0	20
Corruption	Low	5.0	0	10
Political stability	High	10.0	0	20
Economic growth	High	10.0	0	20
Unemployment	Low	5.0	0	10
Inflation	Low	5.0	0	10
Interest rates	Low	5.0	0	10
Stock market	High	10.0	0	20
Bond market	High	10.0	0	20
Real estate market	High	10.0	0	20
Commodity market	High	10.0	0	20
Energy market	High	10.0	0	20
Food market	High	10.0	0	20
Healthcare market	High	10.0	0	20
Education market	High	10.0	0	20
Technology market	High	10.0	0	20
Media market	High	10.0	0	20
Entertainment market	High	10.0	0	20
Travel market	High	10.0	0	20
Transportation market	High	10.0	0	20
Construction market	High	10.0	0	20
Manufacturing market	High	10.0	0	20
Retail market	High	10.0	0	20
Food and beverage market	High	10.0	0	20
Pharmaceutical market	High	10.0	0	20
Automotive market	High	10.0	0	20
Aerospace market	High	10.0	0	20
Defense market	High	10.0	0	20
Energy market	High	10.0	0	20
Healthcare market	High	10.0	0	20
Education market	High	10.0	0	20
Technology market	High	10.0	0	20
Media market	High	10.0	0	20
Entertainment market	High	10.0	0	20
Travel market	High	10.0	0	20
Transportation market	High	10.0	0	20
Construction market	High	10.0	0	20
Manufacturing market	High	10.0	0	20
Retail market	High	10.0	0	20
Food and beverage market	High	10.0	0	20
Pharmaceutical market	High	10.0	0	20
Automotive market	High	10.0	0	20
Aerospace market	High	10.0	0	20
Defense market	High	10.0	0	20

Amino acid sequence of zFP506 Yellow mutant

Figure 13

MAQSKHGLTKEMTMKYRMEGCVDPGHKFVITGEGIGYPFKGKQAINLCVVEGGPLPFAEDILSAGFKYGDRVFTEYPQDI  
VDYFKNSCPAGYTWNRSFLFEDGAVCICNADITVSVEENCVYHESKFYGVNFPADGPMKMTDNWEPSCEKIIPVPRQ  
GILKGDVSMYLLKDGRLRCQFDTVYKAKSVPKMPDWHFIQHKLTREDRSDAKNQKWHLTEHAIASGSALS\*  
(SEQ ID NO:32)

Figure 14

Non-aggregating mutant FP4-NA was generated from zFP538-M128V (humanized version). In comparison with zFP538-M128V, FP4-NA contains two additional amino acid substitutions - K5E and K9T. Also, two accidental nucleotide substitutions were introduced due to PCR mistakes (double underline).

Cloning into pQE30 was done using BamHI and HindIII sites:

```

GGA TCC GCC CAC AGC GAG CAC GGC CTG ACC GAG GAG ATG ACC ATG AAG
BamHI  A  H  S  E  H  G  L  T  E  E  M  T  M  K

TAC CAC ATG GAG GGC TGC GTG AAC GGC CAC AAG TTC GTG ATC ACC GGC
Y  H  M  E  G  C  V  N  G  H  K  F  V  I  T  G

GAG GGC ATC GGC TAC CCC TTC AAG GGC AAG CAG ACC ATC AAC CTG TGC
E  G  I  G  Y  P  F  K  G  K  Q  T  I  N  L  C

GTG ATC GAG GGC GGC CCC CTG CCC TTC AGC GAG GAC ATC CTG AGC GCC
V  I  E  G  G  P  L  P  F  S  E  D  I  L  S  A

GGC TTC AAG TAC GGC GAC CGG ATC TTC ACC GAG TAC CCC CAG GAC ATC
G  F  K  Y  G  D  R  I  F  T  E  Y  P  Q  D  I

GTG GAC TAC TTC AAG AAC AGC TGC CCC GCC GGC TAC ACC TGG GGC CGG
V  D  Y  F  K  N  S  C  P  A  G  Y  T  W  G  R

AGC TTC CTG TTC GAG GAC GGC GCC GTG TGC ATC TGT AAC GTG GAC ATC
S  F  L  F  E  D  G  A  V  C  I  C  N  V  D  I

ACC GTG AGC GTG AAG GAG AAC TGC ATC TAC CAC AAG AGC ATC TTC AAC
T  V  S  V  K  E  N  C  I  Y  H  K  S  I  F  N

GGC GTG AAC TTC CCC GCC GAC GGC CCC GTG ATG AAG AAG ATG ACC ACC
G  V  N  F  P  A  D  G  P  V  M  K  K  M  T  T

AAC TGG GAG GCC AGC TGC GAG AAG ATC ATG CCC GTG CCT AAG CAG GGC
N  W  E  A  S  C  E  K  I  M  P  V  P  K  Q  G

ATC CTG AAG GGC GAC GTG AGC ATG TAC CTG CTG CTG AAG GAC GGC GGC
I  L  K  G  D  V  S  M  Y  L  L  L  K  D  G  G

CGG TAC CGG TGC CAG TTC GAC ACC GTG TAC AAG GCC AAG AGC GTG CCC
R  Y  R  C  Q  F  D  T  V  Y  K  A  K  S  V  P

AGC AAG ATG CCC GAG TGG CAC TTC ATC CAG CAC AAG CTG CTG CGG GAG
S  K  M  P  E  W  H  F  I  Q  H  K  L  L  R  E

GAC CGG AGC GAC GCC AAG AAC CAG AAG TGG CAG CTG ACC GAG CAC GCC
D  R  S  D  A  K  N  Q  K  W  Q  L  T  E  H  A

ATC GCC TTC CCC AGC GCC CTG GCC TGA AAGCTT
I  A  F  P  S  A  L  A  * HindIII (SEQ ID NOS: 33-34)

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10006922 "120404"

All mutants are derived from drFP583 (called "pink" or FP6.) by random mutagenesis

Mutant: **E5 = V105A, S197T** Phenotype: in *E.coli* seen as Green overnight, matures to Red over 24h at 37°C (final peaks ratio Red vs. Green is 75:25); folding is faster t

Mutant: **E83 = N42H, V71A, I180V** Phenotype: always has two almost equal peaks Green & Red; folding is the same as for **E8**

Mutant: **E57 = V105A, I161T, S197A** Phenotype: at common is like **E5up** but folding is more faster (no more that 8-10h) Very small Green peak at final point of maturation (less that 5%)

Mutant: **AG4 = V71M, V105A, S197T** Phenotype: Very bright Green, no Red at all (even at the beginning); folding is faster than **E5** (no more that 16h)

1	Met	Arg	Ser	Ser	Lys	Asn	Val	Ile	Lys	Glu	Phe	Met	Arg	Phe	Lys	Val	16
1	ATG	CGC	TCC	TCC	AAG	AAC	GTC	ATC	AAG	GAG	TTC	ATG	CGC	TTC	AAG	GTG	48

His (CAC) for E8 and E83

49	Thr	Lys	Gly	Gly	Pro	Leu	Pro	Phe	Ala	Trp	Asp	Ile	Leu	Ser	Pro	Gln	64
145	ACC	AAG	GGC	GGC	CCC	CTG	CCC	TTC	GCC	TGG	GAC	ATC	CTG	TCC	CCC	CAG	192

**Met** (ATG) for AG4 and AG45/**Ala** (GCG) for E83

81	Asp	Tyr	Lys	Lys	Leu	Ser	Phe	Pro	Glu	Gly	Phe	Lys	Trp	Glu	Arg	Val	96
241	GAC	TAC	AAG	AAG	CTG	TCC	TTC	CCC	GAG	GGC	TTC	AAG	TGG	GAG	CGC	GTG	288

Ala (GCG) - for E5, E57, AG4 and AG45

His (CAC) -for AG45

129 Phe Pro Ser Asp Gly Pro Val Met Gln Lys Lys Thr Met Gly Trp Glu 144  
385 TTC CCC TCC GAC GGC CCC GTG ATG CAG AAG AAG ACC ATG GGC TGG GAG 432

Thr (ACC) for E57

Val (GTC) for E83

**Thr**(ACC) for E5, AG4 and AG45/**Ala**(GCC) for E57

209 Thr Ile Val Glu Gln Tyr Glu Arg Thr Glu Gly Arg His His Leu Phe Leu \*\*\* 229  
625 ACC ATC GTG GAG CAG TAC GAG CGC ACC GAG GGC CGC CAC CAC CTG TTC CTG TAA 678  
(SEQ ID NO:11 & 12)

FIGURE 16

Nucleic acid sequence of humanized drFP583

ATGGTGCCTCCTCCAAGAACGTCATCAAGGAGTTCATGCGCTTCAAGGTGCGCATGG  
AGGGCACCGTGAACGGCCACGAGTTCGAGATCGAGGGCGAGGGCGAGGGCCGCCCC  
TACGAGGGCCACAACACCGTGAAGCTGAAGGTGACCAAGGGCGGCCCCCTGCCCTTC  
GCCTGGGACATCCTGTCCCCCAGTTCAGTACGGCTCCAAGGTGTACGTGAAGCACC  
CCGCCGACATCCCCGACTACAAGAAGCTGTCTTCCCCGAGGGGCTTCAAGTGGGAGC  
GCGTGATGAACTTCGAGGACGGCGGCGTGGTGACCGTGACCCAAGACTCCTCCCTGC  
AGGACGGCTGCTTCATCTACAAGGTGAAGTTCATCGGCGTGAAGTTCCTCCCTCCGACGG  
CCCCGTAATGCAGAAGAAGACCATGGGCTGGGAGGCCTCCACCGAGCGCCTGTACCC  
CCGCGACGGCGTGCTGAAGGGCGAGATCCACAAGGCCCTGAAGCTGAAGGACGGCG  
GCCACTACCTGGTGGAGTTCAAGTCCATCTACATGGCCAAGAAGCCCGTGACGCTGCC  
CGGCTACTACTACGTGGACTCCAAGCTGGACATCACCTCCCACAACGAGGACTACAC  
CATCGTGGAGCAGTACGAGCGCACCGAGGGCCGCCACCACCTGTTCTGTAG (SEQ ID  
NO:35)

Figure 17

DNA sequence (ORF) of E5-NA

ATGGCCTCCTCCGAGAACGTCATCACCGAGTTCATGCGCTTCAAGGTGCGCATGGAGGGCACCGTGAACGGCCACGAGT  
TCGAGATCGAGGGCGAGGGCGAGGGCCGCCCTACGAGGGCCACAACACCGTGAAGTTGAAGGTGACCAAGGGCGGCCC  
CCTGCCCTTCGCCTGGGACATCCTGTCCCCCAGTTCAGTACGGCTCCAAGGTGTACGTGAAGCACCCTCCGACATC  
CCCGACTACAAGAAGCTGTCTTCCCCGAGGGGCTTCAAGTGGGAGCGCGTGATGAACTTCGAGGACGGCGGCGTGGCGA  
CCGTGACCCAGGACTCCTCCCTGCAGGACGGCTGCTTCATCTACAAGGTGAAGTTCATCGGCGTGAAGTTCCTCCCTCCGA  
CGCCCCCGTGATGCAGAAGAAGACCATGGGCTGGGAGGCCCTCCACCGAGCGCCTGTACCCCCGCGACGGCGTGCTGAAG  
GGCGAGATCCACAAGGCCCTGAAGCTGAAGGACGGCGGCCACTACCTGGTGGAGTTCAAGTCCATCTACATGGCCAAGA  
AGCCCGTGACGCTGCCCGGCTACTACTACGTGGACACCAAGCTGGACATCACCTCCCACAACGAGGACTACACCATCGT  
GGAGCAGTACGAGCGCACCGAGGGCCGCCACCACCTGTTCTGTAA (SEQ ID NO:36)

Figure 18

ATGGTGCCTCCTCCAAGAA CGTCATCAAG GAGTTCATGC GCTTCAAGGT  
GCGCATGGAGGGCACCGTGA ACGGCCACGA GTTCGAGATC GAGGGCGAGG GCGAGGGCCG  
CCCCTACGAG GGCCACAACA CCGTGAAGCT GAAGGTGACC AAGGGCGGCC CCCTGCCCTT  
CGCCTGGGAC ATCCTGTCCC CCCAGTTCCA GTACGGCTCC AAGGTGTACG TGAAGCACCC  
CGCCGACATC CCCGACTACA AGAAGCTGTC CTTCCCCGAG GGCTTCAAGT GGGAGCGCGT  
GATGAACTTCGAGGACGGCG GCGTGGCGAC CGTGACCAA GACTCCTCCC TGCAGGACGG  
CTGCTTCATC TACAAGGTGA AGTTCATCGG CGTGAAGTTC CCCTCCGACG GCCCCGTAAT  
GCAGAAGAAG ACCATGGGCT GGGAGGCCTC CACCGAGCGC CTGTACCCCC GCGACGGCGT  
GCTGAAGGGC GAGACCCACA AGGCCCTGAA GCTGAAGGAC GGCGGCCACT ACCTGGTGGG  
GTTCAAGTCC ATCTACATGG CCAAGAAGCC CGTGCAGCTG CCCGGCTACT ACTACGTGGA  
CGCCAAGCTG GACATCACCT CCCACAACGA GGAATACACC ATCGTGGAGC AGTACGAGCG  
CACCGAGGGCCGCCACCACC TGTTCTGTGA G (SEQ ID NO:37)

1000692.120401

Figure 19.

Nucleic acid sequence FP6 (E57)-NA

ATGGCCTCCTCCGAGAACGTCATCACCGAGTTCATGCGCTTCAAGGTGCGCATGGAGGGCACCGTGA  
ACGGCCACGAGTTCGAGATCGAGGGCGAGGGCGAGGGCCGCCCTACGAGGGCCACAACACCGTG  
AAGCTGAAGGTGACCAAGGGCGGCCCCCTGCCCTTCGCTGGGACATCCTGTCCCCCAGTTCAGT  
ACGGCTCCAAGGTGTACGTGAAGCACCCCGCCGACATCCCCGACTACAAGAAGCTGTCCTTCCCCGA  
GGGCTTCAAGTGGGAGCGCGTGATGAACTTCGAGGACGGCGGCGTGCGGACCGTGACCCAGGACTC  
CTCCCTGCAGGACGGCTGCTTCATCTACAAGGTGAAGTTCATCGGCGTGAAGTTCCTCCCTCCGACGGC  
CCCGTGATGCAGAAGAAGACCATGGGCTGGGAGGCCTCCACCGAGCGCCTGTACCCCCGCGACGGC  
GTGCTGAAGGGCGAGACCCACAAGGCCCTGAAGCTGAAGGACGGCGGCCACTACCTGGTGGAGTTC  
AAGTCCATCTACATGGCCAAGAAGCCCGTGACGCTGCCCGGCTACTACTACGTGGACGCCAAGCTGG  
ACATCACCTCCACAACGAGGACTACACCATCGTGGAGCAGTACGAGCGCACCGAGGGCCGCCACCA  
CCTGTTCTG (SEQ ID NO:38)

T04027-22690007





ATG	GCC	TCC	<b>TTC</b>	CTG	AAG	AAG	<b>ACC</b>	ATG	CCC	TTC	<b>AAG</b>	ACC	ACC	ATC	GAG
M	A	S	<u>F</u>	L	K	K	<u>T</u>	M	P	F	<u>K</u>	T	T	I	E
GGC	ACC	GTG	AAC	GGC	CAC	TAC	TTC	AAG	TGC	ACC	GGC	AAG	GGC	GAG	GGC
G	T	V	N	G	H	Y	F	K	C	T	G	K	G	E	G
AAC	CCC	<b>TTC</b>	GAG	GGC	ACC	CAG	GAG	ATG	<b>AAG</b>	ATC	GAG	GTG	ATC	GAG	GGC
N	P	<u>F</u>	E	G	T	Q	E	M	<u>K</u>	I	E	V	I	E	G
GGC	CCC	CTG	CCC	TTC	GCC	TTC	CAC	ATC	CTG	TCC	ACC	TCC	TGC	ATG	TAC
G	P	L	P	F	A	F	H	I	L	S	T	S	C	M	Y
GGC	TCC	AAG	GCC	TTC	ATC	<b>AAG</b>	TAC	<b>GTG</b>	TCC	GGC	ATC	CCC	GAC	TAC	TTC
G	S	K	A	F	I	K	Y	<u>V</u>	S	G	I	P	D	Y	F
AAG	CAG	TCC	<b>TTC</b>	CCC	GAG	GGC	TTC	ACC	TGG	GAG	CGC	ACC	ACC	ACC	TAC
K	Q	S	<u>F</u>	P	E	G	F	T	W	E	R	T	T	T	Y
GAG	GAC	GGC	GGC	<b>TTC</b>	CTG	ACC	GCC	CAC	CAG	GAC	ACC	TCC	CTG	GAC	GGC
E	D	G	G	<u>F</u>	L	T	A	H	Q	D	T	S	L	D	G
GAC	TGC	CTG	GTG	TAC	AAG	GTG	AAG	ATC	CTG	GGC	AAC	AAC	TTC	CCC	GCC
D	C	L	V	Y	K	V	K	I	L	G	N	N	F	P	A
GAC	GGC	CCC	GTG	ATG	CAG	AAC	AAG	GCC	GGC	CGC	TGG	GAG	CCC	TCC	ACC
D	G	P	V	M	Q	N	K	A	G	R	W	E	P	S	T
GAG	ATC	GTG	TAC	GAG	GTG	GAC	GGC	GTG	CTG	CGC	GGC	CAG	TCC	CTG	ATG
E	I	V	Y	E	V	D	G	V	L	R	G	Q	S	L	M
GCC	CTG	<b>AAG</b>	TGC	CCC	<u>GGC</u>	<u>GGC</u>	<u>CGC</u>	CAC	CTG	ACC	TGC	CAC	CTG	CAC	ACC
A	L	<u>K</u>	C	P	G	G	R	H	L	T	C	H	L	H	T
ACC	TAC	CGC	TCC	AAG	AAG	CCC	GCC	TCC	GCC	CTG	AAG	ATG	CCC	GGC	TTC
T	Y	R	S	K	K	P	A	S	A	L	K	M	P	G	F
CAC	TTC	GAG	GAC	CAC	CGC	ATC	GAG	<b>ATC</b>	<b>ATG</b>	GAG	GAG	GTG	GAG	AAG	GGC
H	F	E	D	H	R	I	E	<u>I</u>	<u>M</u>	E	E	V	E	K	G
AAG	TGC	TAC	AAG	CAG	TAC	GAG	GCC	GCC	GTG	GGC	CGC	TAC	TGC	<b>GAC</b>	GCC
K	C	Y	K	Q	Y	E	A	A	V	G	R	Y	C	<u>D</u>	A
GCC	CCC	TCC	AAG	CTG	GGC	CAC	AAC	TgA							
A	P	S	K	L	G	H	N	*							

(SEQ ID NO:41 & 42)

(SEQ ID NO:41 & 42)

Figure 22

## Sequence of humanized 6/9 hybrid gene and 6/9-Q3 mutant

for 6/9-2G and 6/9-Q3 CAG(Q)																	
1	ATG	AGC	TGC	AGC	AAG	AAC	GTG	ATC	AAG	GAG	TTC	ATG	CGG	TTC	<b>AAG</b>	GTG	48
1	M	S	C	S	K	N	V	I	K	E	F	M	R	F	<u>K</u>	V	16
49	CGG	ATG	GAG	GGC	ACC	GTG	AAC	GGC	CAC	GAG	TTC	GAG	ATC	AAG	GGC	GAG	96
17	R	M	E	G	T	V	N	G	H	E	F	E	I	K	G	E	32
97	GGC	GAG	GGC	CGG	CCC	TAC	GAG	GGC	CAC	TGC	AGC	GTG	AAG	CTC	ATG	GTG	144
33	G	E	G	R	P	Y	E	G	H	C	S	V	K	L	M	V	48
145	ACC	AAG	GGC	GGC	CCC	CTC	CCC	TTC	GCC	TTC	GAC	ATC	CTC	AGC	CCC	CAG	192
49	T	K	G	G	P	L	P	F	A	F	D	I	L	S	P	Q	64
193	TTC	CAG	TAC	GGC	AGC	AAG	GTG	TAC	GTG	AAG	CAC	CCC	GCC	GAC	ATC	CCC	240
65	F	Q	Y	G	S	K	V	Y	V	K	H	P	A	D	I	P	80
ATG(M) for 6/9-Q3																	
241	GAC	TAC	<b>AAG</b>	AAG	CTC	AGC	TTC	CCC	GAG	GGC	TTC	AAG	TGG	GAG	CGG	GTG	288
81	D	Y	<u>K</u>	K	L	S	F	P	E	G	F	K	W	E	R	V	96
289	ATG	AAC	TTC	GAG	GAC	GGC	GGC	GTG	GTG	ACC	GTG	AGC	CAG	GAC	AGC	AGC	336
97	M	N	F	E	D	G	G	V	V	T	V	S	Q	D	S	S	112
337	CTC	AAG	GAC	GGC	TGC	TTC	ATC	TAC	GAG	GTG	AAG	TTC	ATC	GGC	GTG	AAC	384
113	L	K	D	G	C	F	I	Y	E	V	K	F	I	G	V	N	128
385	TTC	CCC	AGC	GAC	GGC	CCC	GTG	ATG	CAG	CGG	CGG	ACC	CGG	GGC	TGG	GAG	432
129	F	P	S	D	G	P	V	M	Q	R	R	T	R	G	W	E	144
433	GCC	AGC	AGC	GAG	CGG	CTC	TAC	CCC	CGG	GAC	GGC	GTG	CTC	AAG	GGC	GAC	480
145	A	S	S	E	R	L	Y	P	R	D	G	V	L	K	G	D	160
481	ATC	CAC	ATG	GCC	CTC	CGG	CTC	GAG	GGC	GGC	GGC	CAC	TAC	CTC	GTG	GAG	528
161	I	H	M	A	L	R	L	E	G	G	G	H	Y	L	V	E	176
529	TTC	AAG	AGC	ATC	TAC	ATG	GCC	AAG	AAG	CCC	GTG	CAG	CTC	CCC	GGC	TAC	576
177	F	K	S	I	Y	M	A	K	K	P	V	Q	L	P	G	Y	192
577	TAC	TAC	GTG	GAC	AGC	AAG	CTC	GAC	ATC	ACC	AGC	CAC	AAC	GAG	GAC	TAC	624
193	Y	Y	V	D	S	K	L	D	I	T	S	H	N	E	D	Y	208
TCC(S) for 6/9-2G and 6/9-Q3																	
625	ACC	ATC	GTG	GAG	CAG	TAC	GAG	CGG	<b>ACC</b>	GAG	GGC	CGG	CAC	CAC	CTC	TTC	672
209	T	I	V	E	Q	Y	E	R	<u>T</u>	E	G	R	H	H	L	F	224
673	CTC	TGA															678
225	L	*															226

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